

SEQUENCE LISTING

<110> Busfield, Samantha J.

<120> NOVEL MOLECULES OF THE
HERPESVIRUS-ENTRY-MEDIATOR-RELATED
PROTEIN FAMILY AND USES THEREOF

<130> MBIO98-061CP1

<150> US 09/146,950

<151> 1998-09-03

<160> 58

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Homo sapiens

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ttctctttct ctttctcttt ctcttctggc ccacagccgc agcaatggcg ctgagttcct      240
ctgctggagt tcctcctgct agctgggttc ccgagctgcc ggtctgagcc tgaggc atg      299
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Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val
      35                      40                      45

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Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu
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Patent 6,646,666

63246560

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Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
60 65 70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
75 80 85 90
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
95 100 105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
110 115 120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
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Leu
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ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca 144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
35 40 45
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag 192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
50 55 60
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca 240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
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Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
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caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
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agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
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Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
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agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
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Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	
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Leu	

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Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His	
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Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val	
100 105 110	
Gln Lys Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro	
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 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
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 gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
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 -5 1 5 10
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
 15 20 25
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro

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Arg	Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile		
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Ser	Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr		
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Leu	Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu		
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Ser	Leu	Val	Ile	Val	Ile	Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys		
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Val	Lys	Arg	Arg	Lys	Pro	Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser		
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5 10 15															
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Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro															
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tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg		440													
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 Met Glu Pro
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cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac 163
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 Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser
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gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc	307
Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys	
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Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu	
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Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly	
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Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln	
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Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys	
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 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
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 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
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 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
 60 65 70
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
 75 80 85 90
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
 95 100 105
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
 110 115 120
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
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Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	
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Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro			
65	70	75	80
ggc acc tac att gcc cac ctg aat ggc cta agc aag tgt ctg cag tgc			288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys			
85	90	95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc			336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser			
100	105	110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc			384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile			
115	120	125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc			432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser			
130	135	140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc			480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr			
145	150	155	160
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg			528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu			
165	170	175	
gag gaa tgt cag cac cag acc aat tgg cct aat cat atg tgt gaa aag			576
Glu Glu Cys Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys			
180	185	190	
aag aaa gcc aag ggg			591
Lys Lys Ala Lys Gly			
195			

<210> 20
 <211> 159
 <212> PRT
 <213> Homo sapiens

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 Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His
 35 40 45
 Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala
 50 55 60

Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val
65 70 75 80
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His
85 90 95
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val
100 105 110
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro
115 120 125
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln
130 135 140
Thr Asn Trp Pro Asn His Met Cys Glu Lys Lys Lys Ala Lys Gly
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<210> 21
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(38)

<400> 21
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Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10
Pro Cys Tyr Ala Pro Ala
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<210> 22
<211> 114
<212> DNA
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<220>
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<222> (1)...(114)

<400> 22
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1 5 10 15
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Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
20 25 30
ccc tgc tac gcc cca gct 114
Pro Cys Tyr Ala Pro Ala
35

<210> 23
<211> 34
<212> PRT
<213> Homo sapiens

RefSeq: NC_004660

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 Val Cys

<210> 24
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 24
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 1 5 10 15
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
 20 25 30
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
 35 40

<210> 25
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 25
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
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 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
 20 25 30
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
 35 40

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 <211> 105
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(105)

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 Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly
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 aca gtg tgt 105
 Thr Val Cys
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<210> 27
 <211> 126
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(126)

<400> 27

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 1 5 10 15

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg 96
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
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aac tgc tcc agg aca gag aac gcc gtg tgt 126
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
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<210> 28
 <211> 126
 <212> DNA
 <213> Homo sapiens

<220>
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<400> 28

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gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
 20 25 30

gga ggc acc gag agt cag gac acc ctg tgt 126
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
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<210> 29
 <211> 2313
 <212> DNA
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<220>
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 <222> (85)...(642)

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Met Glu Pro Pro Gly Asp Trp Gly Pro	
1 5	
cct ccc tgg aga tcc acc ccc aga acc gac gtc tgc agg ctg gtg ctg	159
Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val Ser Arg Leu Val Leu	
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tat ctc acc ttc ctg gga gcc ccc tgc tac gcc cca gct ctg ccg tcc	207
Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser	
30 35 40	
tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag tgc	255
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys	
45 50 55	
agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc aca	303
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr	
60 65 70	
gtg tgt gaa ccc tgc cct cca ggc acc tac att gcc cac ctc aat ggc	351
Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly	
75 80 85	
cta agc aag tgt ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg	399
Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu	
90 95 100 105	
cgc gcg agc cgg aac tgc tcc agg aca gag aac gcc gtg tgt ggc tgc	447
Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val Cys Gly Cys	
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agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc gcg	495
Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala Ala	
125 130 135	
tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag gga	543
Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys Gly	
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ggc acc gag agt cag gac acc ctg tgt cag aac tgc ccc ccg ggg acc	591
Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro Pro Gly Thr	
155 160 165	
ttc tct ccc aat ggg acc ctg gag gaa tgt cag cac cag acc aaa aag	639
Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln Thr Lys Lys	
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<210> 30
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(38)

<400> 30

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-20 -15 -10
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
-5 1 5 10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
15 20 25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
30 35 40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
60 65 70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
75 80 85 90
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
95 100 105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
110 115 120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
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Glu Glu Cys Gln His Gln Thr Lys Lys Ala
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<210> 31
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(558)

<400> 31

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aga acc gac gtc tgc agg ctg gtg ctg tat ctc acc ttc ctg gga gcc	96
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	
20 25 30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca	144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	
35 40 45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag	192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys	
50 55 60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca	240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	
65 70 75 80	
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc	288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
85 90 95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
100 105 110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
115 120 125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc	432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
130 135 140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	
145 150 155 160	
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg	528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	

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 Glu Glu Cys Gln His Gln Thr Lys Lys Ala
 180 185

558

<210> 32
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 32

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 Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu
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 Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His
 35 40 45
 Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala
 50 55 60
 Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val
 65 70 75 80
 Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His
 85 90 95
 Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val
 100 105 110
 Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro
 115 120 125
 Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln
 130 135 140
 Thr Lys Lys Ala
 145

<210> 33
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(38)

<400> 33

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 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 -20 -15 -10
 Pro Cys Tyr Ala Pro Ala
 -5

<210> 34
 <211> 114
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(114)

<400> 34
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 1 5 10 15

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 ccc tgc tac gcc cca gct 114
 Pro Cys Tyr Ala Pro Ala
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<210> 35
 <211> 34
 <212> PRT
 <213> Homo sapiens

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<210> 36
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 36
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 20 25 30
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
 35 40

<210> 37
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 37
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 20 25 30
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
 35 40

<210> 38
 <211> 105
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(105)

<400> 38

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1 5 10 15

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Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly
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aca gtg tgt 105
Thr Val Cys
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<210> 39

<211> 126

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)...(126)

<400> 39

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1 5 10 15

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg 96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
20 25 30

aac tgc tcc agg aca gag aac gcc gtg tgt 126
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<211> 126

<212> DNA

<213> Homo sapiens

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<222> (1)...(126)

<400> 40

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gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag	96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys	
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Met Glu Pro Pro	
1	
gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac gtc	162
Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val	
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ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc tgc tac gcc	210
Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala	
25 30 35	
cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg ggc tcc gag	258
Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu	
40 45 50	
tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg	306
Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly	
55 60 65	
gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc acc tac att	354
Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile	
70 75 80	
gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa atg tgt gac	402
Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp	
85 90 95 100	
cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg aca gag aac	450
Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn	
105 110 115	
gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg	498
Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly	
120 125 130	
gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag	546

Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln	
135 140 145	
agg gtg cag aag gga ggc acc gag agt cag gac acc ctg tgt cag aac	594
Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn	
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Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln	
165 170 175 180	
cac cag acc aag tgc agc tgg ctg gtg acg aag gcc gga gct ggg acc	690
His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr	
185 190 195	
agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg agc ctc gtc atc	738
Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile	
200 205 210	
gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt gtg aaa aga aga	786
Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys Val Lys Arg Arg	
215 220 225	
aag cca agg ggt gat gta gtc aag gtg atc gtc tcc gtc cag gta ttg	834
Lys Pro Arg Gly Asp Val Lys Val Ile Val Ser Val Gln Val Leu	
230 235 240	
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Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser His Leu Pro Ser	
245 250 255 260	
ccc cgc tgg ggc tgg tgt ttc tgg tgt aca tgg tgg ggg ctc cca gtt	930
Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp Gly Leu Pro Val	
265 270 275	
ctc tgagggtcct gagtctttca agtacagcca cggtagctca ggaaagaacc	983
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gtgagggcct ggggcctctg ttctgctgtg gcctgagctc cccagagtcc tgaggaggag	1463
cgccagttgc cctcgtctca cagaccacac acccagccct cctgggccag cccagagggc	1523
ccttcagacc ccagctgtct gcgcgtctga ctcttgtggc ctcagcagga caggccccgg	1583
gcaactgcctc acagccaagg ctggactggg ttggctgcag tgtggtgttt agtggatacc	1643
acatcggaag tgattttcta aattggattt gaattcggct cctgttttct atttgtcatg	1703
aaacagtgtg tttggggaga tgctgtggga ggatgtaaat atcttgtttc tcctcaaaaa	1763
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1823
agggcggccg c	1834

<210> 42
<211> 277

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(38)

<400> 42

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 -35 -30 -25
 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 -20 -15 -10
 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
 -5 1 5 10
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
 15 20 25
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
 30 35 40
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
 45 50 55
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
 60 65 70
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
 75 80 85 90
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
 95 100 105
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
 110 115 120
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
 125 130 135
 Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
 140 145 150
 Gly Ala Gly Thr Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
 155 160 165 170
 Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
 175 180 185
 Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
 190 195 200
 Val Gln Val Leu Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser
 205 210 215
 His Leu Pro Ser Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp
 220 225 230
 Gly Leu Pro Val Leu
 235

<210> 43
 <211> 831
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(831)

<400> 43

atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro

48

1	5	10	15	
aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc				96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	20	25	30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca				144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	35	40	45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag				192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys	50	55	60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca				240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	65	70	75	80
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc				288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	85	90	95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc				336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	100	105	110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc				384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	115	120	125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc				432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	130	135	140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc				480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	145	150	155	160
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg				528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	165	170	175	
gag gaa tgt cag cac cag acc aag tgc agc tgg ctg gtg acg aag gcc				576
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala	180	185	190	
gga gct ggg acc agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg				624
Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly	195	200	205	
agc ctc gtc atc gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt				672
Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys	210	215	220	
gtg aaa aga aga aag cca agg ggt gat gta gtc aag gtg atc gtc tcc				720
Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser	225	230	235	240

gtc cag gta ttg atc ctc ctc ccc ctc tcc ctc ccc cct cca cct tcc	768
Val Gln Val Leu Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser	
245 250 255	
cac ctc ccc tct ccc cgc tgg ggc tgg tgt ttc tgg tgt aca tgg tgg	816
His Leu Pro Ser Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp	
260 265 270	
ggg ctc cca gtt ctc	831
Gly Leu Pro Val Leu	
275	

<210> 44
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 44

Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys	
1 5 10 15	
Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu	
20 25 30	
Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His	
35 40 45	
Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala	
50 55 60	
Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val	
65 70 75 80	
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His	
85 90 95	
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val	
100 105 110	
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro	
115 120 125	
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln	
130 135 140	
Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr Ser Ser	
145 150 155 160	
Ser His Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile Val Ile	
165 170 175	
Val Cys Ser Thr Val Gly Leu Ile Ile Cys Val Lys Arg Arg Lys Pro	
180 185 190	
Arg Gly Asp Val Val Lys Val Ile Val Ser Val Gln Val Leu Ile Leu	
195 200 205	
Leu Pro Leu Ser Leu Pro Pro Pro Ser His Leu Pro Ser Pro Arg	
210 215 220	
Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp Gly Leu Pro Val Leu	
225 230 235	

<210> 45
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> (1)...(38)

<400> 45
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 -35 -30 -25
 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 -20 -15 -10
 Pro Cys Tyr Ala Pro Ala
 -5

<210> 46
 <211> 114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(114)

<400> 46
 atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 1 5 10 15
 aga acc gac gtc tgc agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 20 25 30
 ccc tgc tac gcc cca gct 114
 Pro Cys Tyr Ala Pro Ala
 35

<210> 47
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 47
 Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys
 1 5 10 15
 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
 20 25 30
 Val Cys

<210> 48
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 48
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1 5 10 15
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
 20 25 30

Thr Val Cys
35

<210> 53
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(126)

<400> 53

tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt	48
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys	
1 5 10 15	

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg	96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg	
20 25 30	

aac tgc tcc agg aca gag aac gcc gtg tgt	126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys	
35 40	

<210> 54
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(126)

<400> 54

tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc	48
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala	
1 5 10 15	

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag	96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys	
20 25 30	

gga ggc acc gag agt cag gac acc ctg tgt	126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys	
35 40	

<210> 55
<211> 66
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (1)...(66)

<400> 55

tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag gaa tgt cag 48
Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln
1 5 10 15

cac cag acc aag tgc agc 66
His Gln Thr Lys Cys Ser
20

<210> 56

<211> 75

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(75)

<400> 56

tgg gta tgg tgg ttt ctc tca ggg agc ctc gtc atc gtc att gtt tgc 48
Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile Val Ile Val Cys
5 10 15

tcc aca gtt ggc cta atc ata tgt gtg 75
Ser Thr Val Gly Leu Ile Ile Cys Val
20 25

<210> 57

<211> 32

<212> DNA

<213> Homo sapiens

<220>

<400> 57

tttttctcga ggccatggag cctcctggag ac 32

<210> 58

<211> 39

<212> DNA

<213> Homo sapiens

<220>

<400> 58

tttttggtatc cgctgctgag aggtctgtct gacttttcc 39